

SEQUENCE LISTING

[110] BANYU PHARMACEUTICAL CO., LTD.

[120] NOVEL GUANOSINE TRIPHOSPHATE (GTP) BINDING PROTEIN-COUPLED RECEPTOR
PROTEINS

[130] B1-103PCT

[140]

[141]

[150] PCT/JP98/05967

[151] 1998-12-25

[150] JP 1999-145661

[151] 1999-05-25

[160] 26

[170] PatentIn Ver. 2.0

[210] 1

[211] 413

[212] PRT

[213] *Rattus norvegicus*

[400] 1

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

275

280

285

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

290

295

300

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

305

310

315

320

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

325

330

335

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

340

345

350

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

·210· 2

·211· 1239

·212· DNA

·213· Rattus norvegicus

·220·

·221· CDS

·222· (1)..(1239)

·400· 2

atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 48

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 96

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc glg gcc aca 144

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc 192

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 240

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 288

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg 336

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gla ctc atc 384

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 432

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 480

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

gig cig gcc ttc cig cig tat ggg cct gcc atc ctg agt tgg gag tac 528

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

cig tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc 576

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc 624

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac 672

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc 720

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

cca gaa ccc cca cca gat gcc cag ccc tgg cca cct cca gct ccc ccc 768

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg 816

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 864

His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

275

280

285

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 912

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

290

295

300

atg aag atg gtc tcc cag agc atc acc cag cgc ttc cgg ctg tgg cgg 960

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

305

310

315

320

gac aag aag gtg gcc aag tgg ctg gcc atc atc gtg agc atc ttt ggg 1008

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

325

330

335

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1056

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

340

345

350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1104

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

ctg tgg gcc aac tgg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag 1239

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

210 3

211 21

212 DNA

213 Artificial Sequence

220

223 Description of Artificial Sequence: Artificially
synthesized primer sequence

400 3

baingccaac cibkccctct c

[210] 4

[211] 20

[212] DNA

[213] Artificial Sequence

[220]

[223] Description of Artificial Sequence: Artificially
synthesized primer sequence

[400] 4

ccataaaaagn nggggttgac

20

[210] 5

[211] 2700

[212] DNA

[213] Rattus norvegicus

[220]

[221] CDS

[222] (351)..(1589)

[400] 5

aattcggcac gaggggcag atcgcggggc gcactcgggt gcgcgcagag ctaggggtgc 60

accgacgcac cgcgggcggc tggagctcgg ctltgcctc gcctgcagcag ccgcgcgcgc 120

cgccccactc cgtcagatt ccgacaccag cccctctcgg ategccctcc tggactctag 180

cccgggctct tgcctcgacc ccgcggacca tgcctcgggc gccccccgga aaaccgggc 240

gggcgaagag ccggcaaaga ttaggctcac gagcgggggc cccaccgggc caccagctc 300

tccgcccgtg ccttgcctgg tgcctccgag ccgtgtgagc ctgctgggce atg gag 356

Met Glu

1

cgc gcg ccg ccc gac ggg ctg atg aac gcg tgc ggc act ctg gcc gga 404

Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly

5

10

15

gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tgc gct gcc tgg acc 452

Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr

20

25

30

gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gla ctg 500

Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu

35

40

45

50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgc agc ctc cgc 548

Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg

55

60

65

acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc 596

Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu

70

75

80

gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc 644

Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly

85

90

95

cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac 692

Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp

100

105

110

tac cta ctg tgt gcc tcc tgg gtc ttc aac atc gta ctc atc agc tat 740

Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr

115

120

125

130

gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag 788

Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln

135

140

145

ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg 836

Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu

150

155

160

gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct 884

Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser

165

170

175

ggc ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac 932

Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr

180

185

190

aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc 980

Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro

195

200

205

210

ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag 1028

Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln

215

220

225

agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa 1076

Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu

230

235

240

ccc cca cca gat gcc cag ccc tgc cca cct cca gct ccc ccc agc tgc 1124

Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys

245

250

255

tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc 1172

Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser

260

265

270

tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc aaa agg 1220

Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg

275 280 285 290

ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc atg aag 1268

Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg Met Lys

295 300 305

atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgg cgg gac aag 1316

Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg Asp Lys

310 315 320

aag glg gcc aag tgg ctg gcc atc atc gtg agc atc ttt ggg ctc tgc 1364

Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys

325 330 335

tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc cat ggc 1412

Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys His Gly

340 345 350

cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt ctg tgg 1460

Arg Cys Ile Pro Asp Tyr Trp TyrGlu Thr Ser Phe Trp Leu Leu Trp

355 360 365 370

gcc aac tgg gcc glc aac ccc glc ctc tac cca ctg tgc cac tac agc 1508

Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser

375

380

385

ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc 1556

Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val

390

395

400

cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg ccccaccctt 1609

Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg gggcccctgt 1669

ccatgtctcg ctccaaatgc catggcgggc tcttagatca tcaaccccg agtggggtag 1729

catggcaggt gggccaagag ccttagttgg tggagctaga gtgtgtctgt tagctctgcc 1789

gccacattct ccttcaccac acagaagaga caatccagga gtcccaggca tgccttcac 1849

ctacacacac acacacacac acacacacac acacaccaca gtgcagtgcc agtgaatgcc 1909

ccctttgcat atttagttgt tgggtgtctc cctaatgcaa acctcgggtgt gtgtctcccg 1969

ctccggccct ggcaatgcgt gcgtgcgcc tgcattgtgt cacaccggc acacaccgc 2029

ccgccacaca ctgtcaacac ctctctctc ccagaagagc tggggacgat gccctttgt 2089

gccactgtct ctltgttlaat cccagagccct ggcctccilat cccccactct cccctcaact 2149
 ctgccccaca aagtgctgag cggctcggga aacttgaagc ttctctgctc ctccactct 2209
 ggatgttttc aggaagaagg aggagaagaa aacacgtctg tgaacttgaat gtcccttggg 2269
 tgtttlaatca agagagacaa aatlgccgag gagctcgggg ctggattggc aggtgtgggc 2329
 tcccaagccc tccctccca gtcctgcagc ttccggctga gccgcgccag ctgcttctgc 2389
 ctgccccgcc cccaggcttg ggacgatggc cctgccccgc ttgccccgtc tglacaaatca 2449
 gaatttgggg gttgggtgggt atggggtaga gcggctcttc actgtgccc t aaaggctctg 2509
 aggtctacag gacagtcagc aggagagcag gcaggccccc gacacctggg aggaatgctt 2569
 tgcctcgtcc tgtgtactca cctcaggctt ctgcatgctc tgcctgccc t gtccccggg 2629
 gtgctgccc tgcctaatgtg aaaacacaaat aaagtgtatt tttttacgga aaaaaaana 2689
 aaaaaaaaaa a 2700

(210) 6

(211) 29

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 6

cgaggtatccg tgaggctccg gtgcccgc

29

· 210 · 7

· 211 · 32

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 7

cgggtaagct tcacgacacc tgaaalggaa ga

32

· 210 · 8

· 211 · 24

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 8

ctttctgcat cccattgtac gtacc

24

· 210 · 9

· 211 · 21

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 9

cttccgccgg gcccttcacca a

21

· 210 · 10

· 211 · 24

· 212 · DNA

· 213 · Artificial Sequence

·220·

·223· Description of Artificial Sequence: Artificially
synthesized primer sequence

·400· 10

acagacacgg cggggctcac

20

·210· 11

·211· 1350

·212· DNA

·213· Homo sapiens

·220·

·221· exon

·222· (280)..(557)

·400· 11

gcactcggct gcgcgttgcg tccggctgca cggtcgcacc ggcagcggct caggctccgg 60

ctctctctcc gctgcagcag ccgcgctgcc ggccccactg ggcctcggtc cgcccccgcc 120

ccccctggca ccgcctgctc tggccccggc cccggccccg cggaccaatc gctgggcgcc 180

cccaggggaa cccgaccggg ccaagggccg gcaaagacga ggcctccggg ccggggcccc 240

tccggccgc ccagctctcg gccggcgccc tggccccgt cccggagccg cgtgagcccg 300

cgggggccatg gagcgcgcgc cgcgcgacgg gccgcctgaac gccttcggggg cgcctggcggg 360

cgaggcggcg gcggcgggcg gggcgcgcgg ctctctggca gccctggaccg cggctgcctgc 420

cgcgcctcatg gcgcctgcctc tctgggccac ggctgcctggc aacgcgcctgg tcatgctcgc 480

cttcctggcc gactcgagcc tccgcaccca gaacaacttc ttcctgcctc acctcgccat 540

ctccgacttc ctgcctggta aatccccagc cctctggccg tggggaccca ggggcgccta 600

gccttgcccg gccagcgggg actggaacac ggacctgggt ggctcccgca ggcacacgcc 660

ccaccagggg acccgccctg ggaagggggc gtcggagcc catggggctg ggggcacagg 720

cgaagttcct tgcacctcag gccctgggac aggggctggg gagagatgc cccgggaagg 780

gacacgggca ctgggcgagg cgcaaggcgc aaaggcagcg ggtgcagctc tggctccctgc 840

gcctlagcca aacaaaggct gcctcggact taggacgcgc ggagggcgca gtggggcgggt 900

ttagagaagg tctgggggag gggacatgga agggggattt ttagagctgt gtgggggaa 960

gggacggctg ggaaggctgg ggttggggga gacgcctgga ggagcctgc ctacagctgc 1020

caggctctgc tgcctggctg ggggcggggc acgcggaggg gccctggagcg ccagacacct 1080

gttggggctg tgagggtgct cccccagacg ctccaagccc gcttggcagt agtagtagcg 1110

gcctggcggct ggcggtcgca accaagtgcc ctctcagcca ggagaaagge ttctccttg 1200

tctaagctga gaccgagggt tgtccagcgc cagggtaggg gctggagtc agcgggggag 1260

gggagaagga aattgtcttc ttctctctt tgagggtgg gagggctgga cagaagtcca 1320

gggaatcccg actccaggct ctggggggtc 1350

· 210 · 12

211 · 448

· 212 · DNA

213 · Homo sapiens

· 220 ·

· 221 · exon

· 222 · (259)..(425)

· 400 · 12

gagctcccca tgcctggatc atccctcccg cccccagccc caggggacac agatagtgt 60

gggagctatg tgggggtgaa ggcctggcggc agggcagagt ttgtggctga caccaggctg 120

agggggiggia agatgaggat ggctagttcc agaaaagcag ccaccaigig acceccaggic 180

ccgccggigti ctgcgcttag gtcctctgti cccctggccc ctggctgcat ggiccacatg 240

tggecciacl ccccacaggc gccctctgca tcccacigta tgtaccctac gtcctgacag 300

gccctggac ctccggccgg gccctctgca agctgiggct ggtagtggac taccctgtgt 360

gcacctccctc tgccttcaac atcgtgccta tcagctacga ccgttccctg tcggtcaccc 420

gagcggigag tccctgggctg cggagctc 448

· 210 · 13

· 211 · 1893

· 212 · DNA

· 213 · Homo sapiens

· 220 ·

· 221 · exon

· 222 · (293)..(1209)

· 400 · 13

gagctcacag ctggtagggg gttgtaaaca ggcagcctag cagagagtga ggttcaggc 60

tgttccagg gagcttctga ggcctcact gagtctggca gggcaccagt ccgggacccc 120

aglggggagg gllagaggaa gggaggggaa agagggaggg agggaggaca ggaggggaaa 180

ggaggagcat tgcigcigag ggaagggccc acataggggc ccacaggcta cgggggcgca 240

cccagcccaa taticctcc gcccgcccc igaccagcct gcccttcctc aggtctcata 300

ccgggcccag cagggtaga cgcggcgggc aglccggaag atgctgctgg tgtgggtgct 360

ggccttcctg ctgtacggac cagccatcct gacigggag tactgtccg ggggcagctc 420

catccccgag ggcctctgct atgccgagtt ctctacaac tggctctcc tcatcaggc 480

tccacctg gattcttta cgccttcct cagctcacc tctttaacc tcagcatcta 540

cctgaacatc cagaggcgca cccgctccg gctggatggg gctcgagagg cagccggccc 600

cgagccccc cccgagggcc agccctcacc acccccaccg cctggctgct ggggctgctg 660

gcagaagggg cacggggagg ccatgccgt gcacaggtaa ggggtgggtg aggcggcgt 720

aggcgtgag gccggggagg cgacctcgg gggtagcgt gggggcggct ccttggttc 780

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gggtcccaag ccatcggtt cctggctc actggagaag ccatgaaga tgggtccca 900

gagcilleace cagcgclile ggcigletcg ggacaggaaa gggccaagt cgcggccgt 960

categlgage atctllgggc tctgctgggc cccatacacg ctcctgaiga tcatccgggc 1020

cgcctgccaat ggccaactgcg tccctgacta ctggtagaa acctcttct ggctcctgtg 1080

ggccaactcg gctgtaacc ctgctctta cctctgtgc caccacagct tccgccgggc 1140

cttcaccaag ctgctctgcc cccagaagct caaaatccag cccacagct ccttgagca 1200

ctgctggaag tgagtgccc accagagct cctcagcca cgcctctctc agcccaggtc 1260

tctlgggcat ctggccctgc tccccctac ccggctcglt cccccagggg tgagccccgc 1320

ctgtctgtg gccctctctt aatgccacgg cagccacct gccatggagg cgccttctg 1380

ggtlggccag agggccctc actggctgga ctggaggctg ggtlgccggc cctgcccccc 1440

acattctggc tccaccggga gggacagct ggaggctcca gacatgctgc ccacccccig 1500

ctggtagcca ccttcgcag ttactgggtg gtgtcttcc caaagcaagc acctgggtgt 1560

gtccaggct tctgccccta gcagttggc ctgcaagtg cacacacctg cacacccctg 1620

cacacacctg cacaccgtc ctctccccgg acaagcccag gacactgct tgcctgctt 1680

ctgtctcttg cataagcctc aggcctggcc ctctcaccce tcttccacc aactctctct 1740

gcccccaaaa gtgtcaaggg gccctaggaa cctcgaagct gtctctctgt tttccattct 1800

gggtgttttc agaaagatga agaagaaaac atgtctgtga acttgatgtt cctgggatgt 1860

ttaatcaaga gagacaaaat tgcctgaggag ctc 1893

210 · 14

211 · 20

212 · DNA

213 · Artificial Sequence

220 ·

223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

400 · 14

tgaacgcctc gggggcgctg 20

210 · 15

211 · 21

212 · DNA

213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 15

gagatggcga ggttagagcag g

21

· 210 · 16

· 211 · 20

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 16

ggctccaagc catcggcgc

20

· 210 · 17

· 211 · 20

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of Artificial Sequence: Artificially

synthesized primer sequence

[400] 17

ctcacctcca gcagtgctcc

20

[210] 18

[211] 20

[212] DNA

[213] Artificial Sequence

[220]

[223] Description of Artificial Sequence: Artificially
synthesized primer sequence

[400] 18

gccttcgcac ccagaacaac

20

[210] 19

[211] 19

[212] DNA

[213] Artificial Sequence

[220]

[223] Description of Artificial Sequence: Artificially
synthesized primer sequence

· 400 · 19

tgcgcctctg gatgttcag

19

· 210 · 20

· 211 · 453

· 212 · PRT

· 213 · Homo sapiens

· 400 · 20

Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu

1

5

10

15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala

225	230	235	240
Gly Pro Glu Pro Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro			
245	250	255	
Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu			
260	265	270	
His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu			
275	280	285	
Ala Thr Leu Gly Gly Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr			
290	295	300	
Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu			
305	310	315	320
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg			
325	330	335	
Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg			
340	345	350	
Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly			
355	360	365	

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys

435

440

445

Lys Lys Thr Cys Leu

450

· 210 · 21

· 211 · 2050

· 212 · DNA

· 213 · Homo sapiens

· 220 ·

· 221 · CDS

· 222 · (271)..(1629)

<400> 21

agagatgtag ggcgccccctt ttagctgcgc acagaacgaa agaactcggt tttcttttaa 60

gtgagtgtag ttgggtgacg ctaggggcgc cctccgcagt gcgcgcagga aagcgcactg 120

aggctgcgga ggcagagctg catgctgggt gcgggaagag gggggctccg tcgcggagtc 180

gctgagtcgg tgccttttta gtagttctg cagctagta tggccccat ttgccttcc 240

actcccgag ccgcgtgagc ctgcggggcc atg gag cgc gcg ccg ccc gac ggg 294

Met Glu Arg Ala Pro Pro Asp Gly

1

5

ccg ctg aac gct tcg ggg gcg ctg gcg ggc gag gcg gcg gcg gcg ggc 342

Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly

10

15

20

ggg gcg cgc ggc ttc tcg gca gcc tgg acc gcg gtg ctg gcc gcg ctc 390

Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu

25

30

35

40

atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg 438

Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met

45

50

55

ctc gcc ttc gtg gcc gac tgg agc ctc cgc acc cag aac aac ttc ttc 486

Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe

60

65

70

ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc 534

Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile

75

80

85

cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgg 582

Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg

90

95

100

ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc 630

Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser

105

110

115

120

tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg tgg gtc 678

Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val

125

130

135

acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca 726

Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala

140

145

150

gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga 774

Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly

155

160

165

cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc 822

Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro

170

175

180

gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc 870

Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile

185

190

195

200

acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc 918

Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe

205

210

215

ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg 966

Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg

220

225

230

ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc 1014

Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala

235

240

245

cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag 1062

Gln Pro Ser Pro Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys

250

255

260

ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg 1110

Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala

265 270 275 280

gcc gta ggc gct gag gcc ggg gag gcg acc ctg ggg ggt ggc ggt ggg 1158

Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly Gly

285 290 295

ggc ggc tcc gtg gct tca ccc acc tcc agc tcc ggc agc tcc tgg agg 1206

Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg

300 305 310

ggc act gag agg ccg cgc tca ctg aag agg ggc tcc aag ccg tgg gcg 1254

Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala

315 320 325

tcc tgg gcc tgg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc 1302

Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe

330 335 340

acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tgg ctg 1350

Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu

345 350 355 360

gcc gtc atc gtg agc atc ttt ggg ctg tgc tgg gcc cca tac acg ctg 1398

Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu

365

370

375

ctg atg atc atc egg gcc gcc tgc cat ggc cac tgc gtc cct gac tac 1446

Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr

380

385

390

igg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tgc gct gtc aac 1494

Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn

395

400

405

cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc egg gcc ttc acc 1542

Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr

410

415

420

aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg 1590

Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu

425

430

435

440

gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat 1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu

445

450

gttccctggga tgttttaatca agagagacaa aattgcctgag gagctcaggg ctggattggc 1699

aggctgtgggc tcccagccc tccctcccctc gctaaaggctt ccggctgagc tgtgccagct 1759

gccttcgccc acccgcctc tgggtcaca ccagccctgg tggccaagcc tgccecggcc 1819

actctgtttg ctacccagg acctctgggg gtgttggga ggagggggcc cggctgggcc 1879

cgagggtccc aaggcgtgca ggggcggicc agaggaggcg ccggggcagg ggcgccttcg 1939

ccatgtgctg tgcaccctg ccacgcctc tgcattgcc tctgctgtg cccgtgcgc 1999

tgccttgcaa accgtgaggt cacaataaag tgtattttt tattggtgct g 2050

[210] 22

[211] 20

[212] DNA

[213] Artificial Sequence

[220]

[223] Description of Artificial Sequence: Artificially
synthesized primer sequence

[400] 22

tgcateccat tgtacgtccc 20

[210] 23

[211] 20

[212] DNA

[213] Artificial Sequence

(220)

(223) Description of Artificial Sequence: Artificially
synthesized primer sequence

(400) 23

atcattagga gcgtgtangg

20

(210) 24

(211) 20

(212) DNA

(213) Artificial Sequence

(220)

(223) Description of Artificial Sequence: Artificially
synthesized primer sequence

(400) 24

tgctctggga caccatcttc

20

(210) 25

(211) 445

(212) PRT

(213) Rattus norvegicus

<400> 25

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115 120 125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130 135 140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145 150 155 160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165 170 175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180 185 190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195 200 205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210 215 220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225 230 235 240

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245 250 255

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260 265 270

His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu

275

280

285

Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr

290

295

300

Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

305

310

315

320

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

325

330

335

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

340

345

350

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

355

360

365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

[210] 26

[211] 1953

[212] DNA

[213] Rattus norvegicus

[220]

[221] CDS

[222] (302)..(1636)

[400] 26

agctaggggt gcaccgacgc accgcggcgg ctggagctcg gctttgctct cgctgcagca 60

gccgcgccgc ccgccccact ccgtcagat tccgacacca gccccctctg gatcgccttc 120

ctggactcta gcccgggctc ttgtccgac ccgcgggacc atgtccggg cgcctcccg 180

aaaaccgggc tgggcgaaga gccggcaaag attaggctca cgagcggggg cccacccgg 240

ccaccagct ctcgccccgt gccctgcccc gctgcccca gccgtgtgag cctgcagggc 300

c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tgc ggc act ctg 349

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1

5

10

15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tgc gct gcc 397

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 445

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgc agc 493

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 541

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 589

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtc 637

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

gta gac tac cta ctg tgt gcc tcc tgc gtc ttc aac atc gta ctc atc 685

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 733

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 781

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 829

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc 877

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc 925

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac 973

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc 1021

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

cca gaa ccc cca cca gat gcc cag ccc tgc cca cct cca gct ccc ccc 1069

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg 1117

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

cac agg tat ggg glg ggt gag gca ggc cct ggt gtt gag gct ggg gag 1165

His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu

275

280

285

gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tgc ccc acc 1213

Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr

290

295

300

tcc agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 1261

Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

305

310

315

320

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 1309

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

325

330

335

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgc cgg 1357

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

340

345

350

gac aag aag gtg gcc aag tgc ctg gcc atc atc gtg agc atc ttt ggg 1405

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

355

360

365

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1453

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1501

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

ctg tgg gcc aac tgc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1549

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1597

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg 1646

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

ccccaccctt ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg 1706

gggccccggg ccatgctcgg ctccaaatgc catggcggcc tcttagatca tcaacccgc 1766

aglgggglag catggcaggt gggccaagag ccctagttgg tggagctaga gigtgctgg 1826

tagctctgcc gcacattctc ctccaccaca cagaagagac aatccaggag tcccaggcat 1886

gcttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag 1946

tgaatgc

1953